OIPE

RAW SEQUENCE LISTING   DATE: 01/15/2002
PATENT APPLICATION: US/10/028,392   TIME: 08:00:13

Input Set : **A:\ES.txt**
Output Set: **N:\CRF3\01152002\J028392.raw**

ENTERED

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     3 <110> APPLICANT: Bristol-Myers Squibb Company
     5 <120> TITLE OF INVENTION: A NOVEL HUMAN LEUCINE-RICH REPEAT CONTAINING PROTEIN
EXPRESSED
     6       PREDOMINATELY IN NERVOUS SYSTEM TISSUES, HLRRNS1
     8 <130> FILE REFERENCE: D0085.np
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/028,392
C--> 10 <141> CURRENT FILING DATE: 2001-12-20
    10 <150> PRIOR APPLICATION NUMBER: US 60/259,479
    11 <151> PRIOR FILING DATE: 2001-01-03
    13 <150> PRIOR APPLICATION NUMBER: US 60/260,616
    14 <151> PRIOR FILING DATE: 2001-01-09
    16 <160> NUMBER OF SEQ ID NOS: 63
    18 <170> SOFTWARE: PatentIn version 3.0
    20 <210> SEQ ID NO: 1
    21 <211> LENGTH: 2450
    22 <212> TYPE: DNA
    23 <213> ORGANISM: homo sapiens
    25 <220> FEATURE:
    26 <221> NAME/KEY: CDS
    27 <222> LOCATION: (549)..(2450)
    29 <400> SEQUENCE: 1
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    32 ctggaaggaa ggaagccagg aaagaaagaa ggaaagaaag gaaggcaaga aggaaggcgg     120
    34 gcggcgggcg agggcgcggg gccggacggc aggcgggcgc gaggcgagga ggcagagcgg     180
    36 cccccccagc cccaccgccg ccgctgcgga agccccctcc ccacccagga gccggggagg     240
    38 ggggagagcg cgagaggctc caggcccggc cgcagccccg ccccccgcgc ctccccgcag     300
    40 cgggccttgc accccaaatt cctgagcctc attggggggg tcctcccccc acgggccggg     360
    42 catgctgccc cccggaagga acccctctcc tcgctcacga tctcgacagg aagccctgga     420
    44 gaactgggga ggcagagacc ccggctggcc ggaggcatgt ggagggggg gcctgggcgc     480
    46 agggagaggc ccagcggaag ccaagccacc aggccccca gcgtccacgc ggagcatgaa     540
    48 cattgagg atg gcg cgt gcc cgc ggc tcc ccg tgc ccc ccg ctg ccg ccc     590
    49         Met Ala Arg Ala Arg Gly Ser Pro Cys Pro Pro Leu Pro Pro
    50          1               5                  10
    52 ggt agg atg tcc tgg ccc cac ggg gca ttg ctc ttc ctc tgg ctc ttc     638
    53 Gly Arg Met Ser Trp Pro His Gly Ala Leu Leu Phe Leu Trp Leu Phe
    54 15              20                  25                  30
    56 tcc cca ccc ctg ggg gcc ggt gga ggt gga gtg gcc gtg acg tct gcc     686
    57 Ser Pro Pro Leu Gly Ala Gly Gly Gly Gly Val Ala Val Thr Ser Ala
    58              35                  40                  45
    60 gcc gga ggg ggc tcc ccg ccg gcc acc tcc tgc ccc gtg gcc tgc tcc     734
    61 Ala Gly Gly Gly Ser Pro Pro Ala Thr Ser Cys Pro Val Ala Cys Ser
    62              50                  55                  60
    64 tgc agc aac cag gcc agc cgg gtg atc tgc aca cgg aga gac ctg gcc     782
    65 Cys Ser Asn Gln Ala Ser Arg Val Ile Cys Thr Arg Arg Asp Leu Ala
    66          65                  70                  75
    68 gag gtc cca gcc agc atc ccg gtc aac acg cgg tac ctg aac ctg caa     830
    69 Glu Val Pro Ala Ser Ile Pro Val Asn Thr Arg Tyr Leu Asn Leu Gln
    70      80                  85                  90
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72 gag aac ggc atc cag gtg atc cgg acg gac acg ttc aag cac ctg cgg      878
73 Glu Asn Gly Ile Gln Val Ile Arg Thr Asp Thr Phe Lys His Leu Arg
74 95                  100             105                 110
76 cac ctg gag att ctg cag ctg agc aag aac ctg gtg cgc aag atc gag      926
77 His Leu Glu Ile Leu Gln Leu Ser Lys Asn Leu Val Arg Lys Ile Glu
78                 115             120             125
80 gtg ggc gcc ttc aac ggg ctg ccc agc ctc aac acg ctg gag ctt ttt      974
81 Val Gly Ala Phe Asn Gly Leu Pro Ser Leu Asn Thr Leu Glu Leu Phe
82                 130             135             140
84 gac aac cgg ctg acc acg gtg ccc acg cag gcc ttc gag tac ctg tcc     1022
85 Asp Asn Arg Leu Thr Thr Val Pro Thr Gln Ala Phe Glu Tyr Leu Ser
86          145             150             155
88 aag ctg cgg gag ctc tgg ctg cgg aac aac ccc atc gag agc atc ccc     1070
89 Lys Leu Arg Glu Leu Trp Leu Arg Asn Asn Pro Ile Glu Ser Ile Pro
90      160             165             170
92 tcc tac gcc ttc aac cgc gtg ccc tcg ctg cgg cgc ctg gac ctg ggc     1118
93 Ser Tyr Ala Phe Asn Arg Val Pro Ser Leu Arg Arg Leu Asp Leu Gly
94 175                 180             185             190
96 gag ctc aag cgg ctg gaa tac atc tcg gag gcg gcc ttc gag ggg ctg     1166
97 Glu Leu Lys Arg Leu Glu Tyr Ile Ser Glu Ala Ala Phe Glu Gly Leu
98                 195             200             205
100 gtc aac ctg cgc tac ctc aac ctg ggc atg tgc aac ctc aag gac atc    1214
101 Val Asn Leu Arg Tyr Leu Asn Leu Gly Met Cys Asn Leu Lys Asp Ile
102             210             215             220
104 ccc aac ctg acg gcc ctg gtg cgc ctg gag gag ctg gag ctg tcg ggc    1262
105 Pro Asn Leu Thr Ala Leu Val Arg Leu Glu Glu Leu Glu Leu Ser Gly
106         225             230             235
108 aac cgg ctg gac ctg atc cgc ccg ggc tcc ttc cag ggt ctc acc agc    1310
109 Asn Arg Leu Asp Leu Ile Arg Pro Gly Ser Phe Gln Gly Leu Thr Ser
110     240             245             250
112 ctg cgc aag ctg tgg ctc atg cac gcc cag gta gcc acc atc gag cgc    1358
113 Leu Arg Lys Leu Trp Leu Met His Ala Gln Val Ala Thr Ile Glu Arg
114 255             260             265             270
116 aac gcc ttc gac gac ctc aag tcg ctg gag gag ctc aac ctg tcc cac    1406
117 Asn Ala Phe Asp Asp Leu Lys Ser Leu Glu Glu Leu Asn Leu Ser His
118             275             280             285
120 aac aac ctg atg tcg ctg ccc cac gac ctc ttc acg ccc ctg cac cgc    1454
121 Asn Asn Leu Met Ser Leu Pro His Asp Leu Phe Thr Pro Leu His Arg
122         290             295             300
124 ctc gag cgc gtg cac ctc aac cac aac ccc tgg cat tgc aac tgc gac    1502
125 Leu Glu Arg Val His Leu Asn His Asn Pro Trp His Cys Asn Cys Asp
126         305             310             315
128 gtg ctc tgg ctg agc tgg tgg ctc aag gag acg gtg ccc agc aac acg    1550
129 Val Leu Trp Leu Ser Trp Trp Leu Lys Glu Thr Val Pro Ser Asn Thr
130     320             325             330
132 acg tgc tgc gcc cgc tgt cat gcg ccc gcc ggc ctc aag ggg cgc tac    1598
133 Thr Cys Cys Ala Arg Cys His Ala Pro Ala Gly Leu Lys Gly Arg Tyr
134 335             340             345             350
136 att ggg gag ctg gac cag tcg cat ttc acc tgc tat gcg ccc gtc atc    1646
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137 Ile Gly Glu Leu Asp Gln Ser His Phe Thr Cys Tyr Ala Pro Val Ile
138                 355                 360                 365
140 gtg gag ccg ccc acg gac ctc aac gtc acc gag ggc atg gct gcc gag    1694
141 Val Glu Pro Pro Thr Asp Leu Asn Val Thr Glu Gly Met Ala Ala Glu
142                 370                 375                 380
144 ctc aaa tgc cgc acg ggc acc tcc atg acc tcc gtc aac tgg ctg acg    1742
145 Leu Lys Cys Arg Thr Gly Thr Ser Met Thr Ser Val Asn Trp Leu Thr
146             385                 390                 395
148 ccc aac ggc acc ctc atg acc cac ggc tcc tac cgc gtg cgc atc tcc    1790
149 Pro Asn Gly Thr Leu Met Thr His Gly Ser Tyr Arg Val Arg Ile Ser
150         400                 405                 410
152 gtc ctg cat gac ggc acg ctt aac ttc acc aac gtc acc gtg cag gac    1838
153 Val Leu His Asp Gly Thr Leu Asn Phe Thr Asn Val Thr Val Gln Asp
154 415                 420                 425                 430
156 acg ggc cag tac acg tgc atg gtg acg aac tca gcc ggc aac acc acc    1886
157 Thr Gly Gln Tyr Thr Cys Met Val Thr Asn Ser Ala Gly Asn Thr Thr
158                 435                 440                 445
160 gcc tcg gcc acg ctc aac gtc tcg gcc gtg gac ccc gtg gcg gcc ggg    1934
161 Ala Ser Ala Thr Leu Asn Val Ser Ala Val Asp Pro Val Ala Ala Gly
162             450                 455                 460
164 ggc acc ggc agc ggc ggg ggc ggc cct ggg ggc agt ggt ggt gtt gga    1982
165 Gly Thr Gly Ser Gly Gly Gly Gly Pro Gly Gly Ser Gly Gly Val Gly
166             465                 470                 475
168 ggg ggc agt ggc ggc tac acc tac ttc acc acg gtg acc gtg gag acc    2030
169 Gly Gly Ser Gly Gly Tyr Thr Tyr Phe Thr Thr Val Thr Val Glu Thr
170         480                 485                 490
172 ctg gag acg cag ccc gga gag gag gcc ctg cag ccg cgg ggg acg gag    2078
173 Leu Glu Thr Gln Pro Gly Glu Glu Ala Leu Gln Pro Arg Gly Thr Glu
174 495                 500                 505                 510
176 aag gaa ccg cca ggg ccc acg aca gac ggt gtc tgg ggt ggg ggc cgg    2126
177 Lys Glu Pro Pro Gly Pro Thr Thr Asp Gly Val Trp Gly Gly Gly Arg
178                 515                 520                 525
180 cct ggg gac gcg gcc ggc cct gcc tcg tct tct acc acg gca ccc gcc    2174
181 Pro Gly Asp Ala Ala Gly Pro Ala Ser Ser Ser Thr Thr Ala Pro Ala
182             530                 535                 540
184 ccg cgc tcc tcg cgg ccc acg gag aag gcg ttc acg gtg ccc atc acg    2222
185 Pro Arg Ser Ser Arg Pro Thr Glu Lys Ala Phe Thr Val Pro Ile Thr
186             545                 550                 555
188 gat gtg acg gag aac gcc ctc aag gac ctg gac gac gtc atg aag acc    2270
189 Asp Val Thr Glu Asn Ala Leu Lys Asp Leu Asp Asp Val Met Lys Thr
190         560                 565                 570
192 acc aaa atc atc atc ggc tgc ttc gtg gcc atc acg ttc atg gcc gcg    2318
193 Thr Lys Ile Ile Ile Gly Cys Phe Val Ala Ile Thr Phe Met Ala Ala
194 575                 580                 585                 590
196 gtg atg ctc gtg gcc ttc tac aag ctg cgc aag cag cac cag ctc cac    2366
197 Val Met Leu Val Ala Phe Tyr Lys Leu Arg Lys Gln His Gln Leu His
198                 595                 600                 605
200 aag cac cac ggg ccc acg cgc acc gtg gag atc atc aac gtg gag gac    2414
201 Lys His His Gly Pro Thr Arg Thr Val Glu Ile Ile Asn Val Glu Asp
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202                   610                 615                  620
204 gag ctg ccc gcc gcc tcg gcc gtg tcc gtg gcc gcc                            2450
205 Glu Leu Pro Ala Ala Ser Ala Val Ser Val Ala Ala
206              625                 630
209 <210> SEQ ID NO: 2
210 <211> LENGTH: 634
211 <212> TYPE: PRT
212 <213> ORGANISM: homo sapiens
214 <400> SEQUENCE: 2
216 Met Ala Arg Ala Arg Gly Ser Pro Cys Pro Pro Leu Pro Pro Gly Arg
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220 Met Ser Trp Pro His Gly Ala Leu Leu Phe Leu Trp Leu Phe Ser Pro
221              20                  25              30
224 Pro Leu Gly Ala Gly Gly Gly Gly Val Ala Val Thr Ser Ala Ala Gly
225              35                  40              45
228 Gly Gly Ser Pro Pro Ala Thr Ser Cys Pro Val Ala Cys Ser Cys Ser
229     50                  55                  60
232 Asn Gln Ala Ser Arg Val Ile Cys Thr Arg Arg Asp Leu Ala Glu Val
233 65                  70                  75                  80
236 Pro Ala Ser Ile Pro Val Asn Thr Arg Tyr Leu Asn Leu Gln Glu Asn
237                  85                  90                  95
240 Gly Ile Gln Val Ile Arg Thr Asp Thr Phe Lys His Leu Arg His Leu
241              100                 105             110
244 Glu Ile Leu Gln Leu Ser Lys Asn Leu Val Arg Lys Ile Glu Val Gly
245              115                 120                 125
248 Ala Phe Asn Gly Leu Pro Ser Leu Asn Thr Leu Glu Leu Phe Asp Asn
249     130                 135                 140
252 Arg Leu Thr Thr Val Pro Thr Gln Ala Phe Glu Tyr Leu Ser Lys Leu
253 145                 150                 155                 160
256 Arg Glu Leu Trp Leu Arg Asn Asn Pro Ile Glu Ser Ile Pro Ser Tyr
257                  165                 170                 175
260 Ala Phe Asn Arg Val Pro Ser Leu Arg Arg Leu Asp Leu Gly Glu Leu
261              180                 185                 190
264 Lys Arg Leu Glu Tyr Ile Ser Glu Ala Ala Phe Glu Gly Leu Val Asn
265              195                 200                 205
268 Leu Arg Tyr Leu Asn Leu Gly Met Cys Asn Leu Lys Asp Ile Pro Asn
269     210                 215                 220
272 Leu Thr Ala Leu Val Arg Leu Glu Glu Leu Glu Leu Ser Gly Asn Arg
273 225                 230                 235                 240
276 Leu Asp Leu Ile Arg Pro Gly Ser Phe Gln Gly Leu Thr Ser Leu Arg
277                  245                 250                 255
280 Lys Leu Trp Leu Met His Ala Gln Val Ala Thr Ile Glu Arg Asn Ala
281              260                 265                 270
284 Phe Asp Asp Leu Lys Ser Leu Glu Glu Leu Asn Leu Ser His Asn Asn
285              275                 280                 285
288 Leu Met Ser Leu Pro His Asp Leu Phe Thr Pro Leu His Arg Leu Glu
289     290                 295                 300
292 Arg Val His Leu Asn His Asn Pro Trp His Cys Asn Cys Asp Val Leu
293 305                 310                 315                 320
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296 Trp Leu Ser Trp Trp Leu Lys Glu Thr Val Pro Ser Asn Thr Thr Cys
297             325             330             335
300 Cys Ala Arg Cys His Ala Pro Ala Gly Leu Lys Gly Arg Tyr Ile Gly
301             340             345             350
304 Glu Leu Asp Gln Ser His Phe Thr Cys Tyr Ala Pro Val Ile Val Glu
305             355             360             365
308 Pro Pro Thr Asp Leu Asn Val Thr Glu Gly Met Ala Ala Glu Leu Lys
309     370             375             380
312 Cys Arg Thr Gly Thr Ser Met Thr Ser Val Asn Trp Leu Thr Pro Asn
313 385             390             395             400
316 Gly Thr Leu Met Thr His Gly Ser Tyr Arg Val Arg Ile Ser Val Leu
317             405             410             415
320 His Asp Gly Thr Leu Asn Phe Thr Asn Val Thr Val Gln Asp Thr Gly
321             420             425             430
324 Gln Tyr Thr Cys Met Val Thr Asn Ser Ala Gly Asn Thr Thr Ala Ser
325             435             440             445
328 Ala Thr Leu Asn Val Ser Ala Val Asp Pro Val Ala Ala Gly Gly Thr
329     450             455             460
332 Gly Ser Gly Gly Gly Gly Pro Gly Gly Ser Gly Gly Val Gly Gly Gly
333 465             470             475             480
336 Ser Gly Gly Tyr Thr Tyr Phe Thr Thr Val Thr Val Glu Thr Leu Glu
337             485             490             495
340 Thr Gln Pro Gly Glu Glu Ala Leu Gln Pro Arg Gly Thr Glu Lys Glu
341             500             505             510
344 Pro Pro Gly Pro Thr Thr Asp Gly Val Trp Gly Gly Gly Arg Pro Gly
345             515             520             525
348 Asp Ala Ala Gly Pro Ala Ser Ser Ser Thr Thr Ala Pro Ala Pro Arg
349     530             535             540
352 Ser Ser Arg Pro Thr Glu Lys Ala Phe Thr Val Pro Ile Thr Asp Val
353 545             550             555             560
356 Thr Glu Asn Ala Leu Lys Asp Leu Asp Asp Val Met Lys Thr Thr Lys
357 ·               565             570             575
360 Ile Ile Ile Gly Cys Phe Val Ala Ile Thr Phe Met Ala Ala Val Met
361             580             585             590
364 Leu Val Ala Phe Tyr Lys Leu Arg Lys Gln His Gln Leu His Lys His
365             595             600             605
368 His Gly Pro Thr Arg Thr Val Glu Ile Ile Asn Val Glu Asp Glu Leu
369     610             615             620
372 Pro Ala Ala Ser Ala Val Ser Val Ala Ala
373 625             630
376 <210> SEQ ID NO: 3
377 <211> LENGTH: 640
378 <212> TYPE: PRT
379 <213> ORGANISM: Homo sapiens
381 <400> SEQUENCE: 3
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386 Arg Phe Asn Arg Ala Leu Phe Asp Pro Leu Leu Val Val Leu Leu Ala
387             20              25              30
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VERIFICATION SUMMARY
PATENT APPLICATION: US/10/028,392

DATE: 01/15/2002
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Input Set : A:\ES.txt
Output Set: N:\CRF3\01152002\J028392.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application No
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date